



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,248A

DATE: 02/11/2003
TIME: 14:35:12

Input Set : A:\10018248a.raw.txt
Output Set: N:\CRF4\02112003\J018248A.raw

3 <110> APPLICANT: EXELIXIS, INC.
5 <120> TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM
AND SCREENING

6 OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METABOLISM

8 <130> FILE REFERENCE: EX99-004C-US

10 <140> CURRENT APPLICATION NUMBER: 10/018,248A

C--> 11 <141> CURRENT FILING DATE: 2002-07-30

13 <150> PRIOR APPLICATION NUMBER: US 60/189,700

14 <151> PRIOR FILING DATE: 2000-03-15

16 <150> PRIOR APPLICATION NUMBER: US 09/332,522

17 <151> PRIOR FILING DATE: 1999-06-14

19 <160> NUMBER OF SEQ ID NOS: 8

21 <170> SOFTWARE: PatentIn version 3.1

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 3419

25 <212> TYPE: DNA

26 <213> ORGANISM: Caenorhabditis elegans

28 <400> SEQUENCE: 1

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33 cgctcgattt tgacatggag cacaactgac aagagcccg accatcacaa caaccggatc 180
35 catcaattcc cggaaatcaa cacagtccgc cacaggaata ttatgatatt gatggtaac 240
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39 gatTTTCCCC gccaaacttt gatctcgccg gaggccgtgg accttctcta gccgccaccc 360
41 aacaattatc tggagaaggt cctgcaagta tgcttaaccc cttacaaaca tctccaccaa 420
43 gtggagggtta ccccccggca gatgcctaca gacctctatc acttgctcaa caactcgccg 480
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47 aaaagaattt cactcatgca atgcttatctt caccacacca tacctcaatg acttctcaac 600
49 catatacaga agccatggga catatcaacg ggtacatgtc tccatacagac caagctcaag 660
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69 caacactacg acgggctatt gaacatatcg aggaggtga acacgagaat caggtgtga 1260
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178 85 90 95
181 Pro Asn Phe Asp Leu Gly Gly Arg Gly Pro Ser Leu Ala Ala Thr
182 100 105 110
185 Gln Gln Leu Ser Gly Glu Gly Pro Ala Ser Met Leu Asn Pro Leu Gln
186 115 120 125
189 Thr Ser Pro Pro Ser Gly Gly Tyr Pro Pro Ala Asp Ala Tyr Arg Pro
190 130 135 140
193 Leu Ser Leu Ala Gln Gln Leu Ala Ala Pro Ala Met Thr Pro His Gln
194 145 150 155 160
197 Ala Ala Ser Leu Phe Val Asn Thr Asn Gly Ile Asp Gln Lys Asn Phe
198 165 170 175
201 Thr His Ala Met Leu Ser Ser Pro His His Thr Ser Met Thr Ser Gln
202 180 185 190
205 Pro Tyr Thr Glu Ala Met Gly His Ile Asn Gly Tyr Met Ser Pro Tyr
206 195 200 205
209 Asp Gln Ala Gln Gly Pro Ser Gly Pro Ser Tyr Tyr Ser Gln His His
210 210 215 220
213 Gln Ser Pro Pro His His His His His His Pro Met Pro Lys Ile
214 225 230 235 240
217 His Glu Asn Pro Glu Gln Val Ala Ser Pro Ser Ile Glu Asp Ala Pro
218 245 250 255
221 Glu Thr Lys Pro Thr His Leu Val Glu Pro Gln Ser Pro Lys Ser Pro
222 260 265 270
225 Gln Asn Met Lys Glu Glu Leu Leu Arg Leu Leu Val Asn Met Ser Pro
226 275 280 285
229 Ser Glu Val Glu Arg Leu Lys Asn Lys Lys Ser Gly Ala Cys Ser Ala
230 290 295 300
233 Thr Asn Gly Pro Ser Arg Ser Lys Glu Lys Ala Ala Lys Ile Val Ile
234 305 310 315 320
237 Gln Glu Thr Ala Glu Gly Asp Glu Asp Glu Asp Asp Glu Asp Ser Asp
238 325 330 335
241 Ser Gly Glu Thr Met Ser Gln Gly Thr Thr Ile Ile Val Arg Arg Pro
242 340 345 350
245 Lys Thr Glu Arg Arg Thr Ala His Asn Leu Ile Glu Lys Lys Tyr Arg
246 355 360 365
249 Cys Ser Ile Asn Asp Arg Ile Gln Gln Leu Lys Val Leu Leu Cys Gly
250 370 375 380
253 Asp Glu Ala Lys Leu Ser Lys Ser Ala Thr Leu Arg Arg Ala Ile Glu
254 385 390 395 400
257 His Ile Glu Glu Val Glu His Glu Asn Gln Val Leu Lys His His Val
258 405 410 415
261 Glu Gln Met Arg Lys Thr Leu Gln Asn Asn Arg Leu Pro Tyr Pro Glu
262 420 425 430
265 Pro Ile Gln Tyr Thr Glu Tyr Ser Ala Arg Ser Pro Val Glu Ser Ser
266 435 440 445
269 Pro Ser Pro Pro Arg Asn Glu Arg Lys Arg Ser Arg Met Ser Thr Thr
270 450 455 460

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273 Thr Pro Met Lys Asn Gly Thr Arg Asp Gly Ser Ser Lys Val Thr Leu
274 465 470 475 480
277 Phe Ala Met Leu Leu Ala Val Leu Ile Phe Asn Pro Ile Gly Leu Leu
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281 Ala Gly Ser Ala Ile Phe Ser Lys Ala Ala Ala Glu Ala Pro Ile Ala
282 500 505 510
285 Ser Pro Phe Glu His Gly Arg Val Ile Asp Asp Pro Asp Gly Thr Ser
286 515 520 525
289 Thr Arg Thr Leu Phe Trp Glu Gly Ser Ile Ile Asn Met Ser Tyr Val
290 530 535 540
293 Trp Val Phe Asn Ile Leu Met Ile Ile Tyr Val Val Val Lys Leu Leu
294 545 550 555 560
297 Ile His Gly Asp Pro Val Gln Asp Phe Met Ser Val Ser Trp Gln Thr
298 565 570 575
301 Phe Val Thr Thr Arg Glu Lys Ala Arg Ala Glu Leu Asn Ser Gly Asn
302 580 585 590
305 Leu Lys Asp Ala Gln Arg Lys Phe Cys Glu Cys Leu Ala Thr Leu Asp
306 595 600 605
309 Arg Ser Leu Pro Ser Pro Gly Val Asp Ser Val Phe Ser Val Gly Trp
310 610 615 620
313 Glu Cys Val Arg His Leu Leu Asn Trp Leu Trp Ile Gly Arg Tyr Ile
314 625 630 635 640
317 Ala Arg Arg Arg Ser Thr Thr Lys Pro Val Ser Val Val Cys Arg
318 645 650 655
321 Ser His Ala Gln Thr Ala Val Leu Tyr His Glu Ile His Gln Leu His
322 660 665 670
325 Leu Met Gly Ile Thr Gly Asn Phe Glu Asp Thr Tyr Glu Pro Ser Ala
326 675 680 685
329 Leu Thr Gly Leu Phe Met Ser Leu Cys Ala Val Asn Leu Ala Glu Ala
330 690 695 700
333 Ala Gly Ala Ser Asn Asp Gly Leu Pro Arg Ala Val Met Ala Gln Ile
334 705 710 715 720
337 Tyr Ile Ser Ala Ser Ile Gln Cys Arg Leu Ala Leu Pro Asn Leu Leu
338 725 730 735
341 Ala Pro Phe Phe Ser Gly Tyr Phe Leu Arg Arg Ala Arg Arg His Val
342 740 745 750
345 Arg Arg Ala Pro Glu His Ser Val Ser His Leu Leu Trp Ile Phe His
346 755 760 765
349 Pro Ala Thr Arg Lys Phe Met Ser Asp Ala Lys Arg Leu Glu His Val
350 770 775 780
353 Leu Ser Ser Lys Gln Lys Gln Leu Arg Phe Gly Ser Phe Val Glu Asp
354 785 790 795 800
357 Glu Gln Leu Ser Pro Leu Ala Arg Ile Arg Thr Thr Leu Lys Val Tyr
358 805 810 815
361 Leu Leu Ser Lys Leu Val Gln Glu Leu Val Gly Gly Asp Glu Ile Phe
362 820 825 830
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366 835 840 845
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378 885 890 895
381 His Val Leu Thr Cys Gly Ile Tyr Trp Arg Ser Asn Lys Asn Glu Leu
382 900 905 910
385 Ala Arg Gln His Tyr Ser Leu Ile Arg Asn Cys Pro Pro Lys Ile Leu
386 915 920 925
389 Thr Asp Asn Leu Gly Leu Ala Val Gly His Ala Leu Cys Ala Arg Lys
390 930 935 940
393 Ile Cys Ile Asp Asp Arg Asp Ser Pro Lys Val Ser Gln Tyr Val Cys
394 945 950 955 960
397 Ile His Thr Lys Lys Ser Leu Glu Ser Leu Arg Leu Phe Ser Thr Ser
398 965 970 975
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402 980 985 990
405 Met Ala Tyr Glu Trp Ile Met Asn Ser Leu Leu Asp Ala Trp Arg Ser
406 995 1000 1005
409 Asn Leu Phe Ala Ser Lys Pro Tyr Trp Thr Gln Ser Phe Lys Gly
410 1010 1015 1020
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414 1025 1030 1035
417 Ala Ile Ile Asn Gly Thr Arg Gly Asp Cys Trp Arg Leu Phe Val
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421 Tyr Glu Leu Thr Cys Arg Met Leu Asn Gly Ala Asn Pro Gln Ala
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426 1070 1075 1080
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447 cgcaagtgc acgttccacac cggaggaccc ccaactgttag aatccgcatac accatcctaa 180
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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1073

Seq#:7; N Pos. 3038,3049

Seq#:8; Xaa Pos. 993

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5